WHAT IS CLAIMED IS:

1. A biologically pure culture of a microorganism strain comprising all of the identifying characteristics of a *Bacillus thuringiensis* strain deposited at the International Depository Authority of Health Canada in Winnipeg under accession number IDAC010201-5, or a mutant thereof derived from said strain.

2. An isolated nucleic acid molecule comprising a polynucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 2;

(b) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 8;

(c) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 12, with the proviso that said nucleotide sequence does not encode the amino acid sequence in SEQ ID NO: 18;

(d) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 13, with the proviso that said nucleotide sequence does not encode the amino acid sequence at positions 232 to 723 of SEQ ID NO: 18;

(e) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 14, with the proviso that said nucleotide sequence does not encode the amino acid sequence in SEQ ID NO: 18;

(f) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence in SEQ ID NO: 15, with the proviso that said nucleotide sequence does not encode the amino acid sequence at positions 232 to 723 of SEQ ID NO: 18;

(g) a nucleotide sequence encoding a polypeptide comprising the complete amino acid sequence of a crystal protein contained in the *Bacillus thuringiensis* strain deposited at the International Depository Authority of Health Canada in Winnipeg under accession number IDAC010201-5;

(h) a nucleotide sequence encoding a crystal protein comprising the complete amino acid sequence in SEQ ID NO: 10;

(i) a nucleotide sequence comprising the sequence set forth in SEQ ID NO: 1;

(j) a nucleotide sequence comprising the sequence set forth in SEQ ID NO: 9;

(k) a nucleotide sequence encoding a crystal protein comprising the sequence set forth in SEQ ID NO: 11;

(l) a nucleotide sequence encoding a crystal protein having at least 94% identity with the complete amino acid sequence in SEQ ID NO: 2, with the proviso that said nucleotide sequence does not encode the amino acid sequence in SEQ ID NO: 18;

(m) a nucleotide sequence encoding a crystal protein having at least 97% identity with the complete amino acid sequence in SEQ ID NO: 8 with the proviso that said nucleotide sequence does not encode the amino acid sequence from position 232 to 723 of SEQ ID NO: 18;

(n) a nucleotide sequence encoding a crystal protein cytotoxic against at least one human cancer cell, said nucleotide sequence having at least 98% identity with the complete sequence set forth in SEQ ID NO: 9, with the proviso that said nucleotide sequence does not encode the amino acid sequence from position 232 to 723 of SEQ ID NO: 18;

(o) a nucleotide sequence completely complementary to

any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i) (j), (k), (l), (m) and (n); and

(p) a nucleotide sequence which hybridizes under high stringency conditions to any of the nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), (h), (i) (j), (k), (l), (m), (n) and (o).

3. An isolated polypeptide comprising a sequence selected from the group consisting of:

(a) an amino acid as set forth in SEQ ID NO: 2;

(b) an amino acid sequence in SEQ ID NO: 8;

(c) an amino acid sequence of a crystal protein contained in the *bacillus thuringiensis* strain in the deposit at the International Depository Authority of Health Canada in Winnipeg under accession number IDAC010201-5;

(d) a crystal protein comprising the amino acid sequence in SEQ ID NO: 10;

(e) a crystal protein having at least 94% identity with the complete amino acid sequence in SEQ ID NO: 2, with the proviso that said crystal protein is not constituted of SEQ ID NO: 18 ;

(f) a crystal protein having at least 97% identity with the complete amino acid sequence in SEQ ID NO: 8, with the proviso that said crystal protein is not constituted the amino acid sequence at positions 232 to 723 of SEQ ID NO: 18;

(g) a crystal protein cytotoxic against at least one human cancer cell and encoded by a nucleotide sequence having at least 98% identity with the complete sequence in SEQ ID NO: 9, with the proviso that said nucleotide sequence does encode the amino acid sequence at positions 232 to 723 of SEQ ID NO: 18.

4. A recombinant vector comprising an isolated nucleotide sequence of claim 2.

5. A recombinant host cell comprising the vector of claim 4.

6. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule according claim 2 in a vector.

7. A recombinant method for producing a cytotoxic polypeptide, comprising culturing said host cell of claim 5 under conditions such that said polypeptide is expressed and recovering said polypeptide.

8. An isolated antibody that binds specifically to a polypeptide of claim 3.

9. A method of modulating the level of cry31Aa2 active protein in a cell comprising a modulation of the level or activity of the sequence SEQ ID NO: 8.

10. A method of using a polypeptide of claim 3 for lysing a human cancer cell.

11. The method as recited in claim 10 wherein the cells are selected from the group consisting of HELA, TCS, HL-60, Jurkat, and Hep-G2 cells.

12. A method of testing the cytotoxicity of a polypeptide as defined in claim 3 against a candidate cancer cell comprising determining the EC50 of the polypeptide on the candidate cell, wherein the polypeptide is

characterized as possessing cytotoxicity against the candidate cell if the EC50 of the polypeptide against the candidate cell is measurably lower than that against a normal T cell.

13. A method for lysing a human cancer cell comprising applying a cytotoxic amount of a polypeptide of claim 3 on a human cancer cell.

14. A method for obtaining a cytotoxic polypeptide comprising cleaving a polypeptide of claim 3 with a protease able to cleave between a residue R and a residue I.

15. A method as in claim 14, where the protease is trypsin.